us09652282.txt

(1) GENERAL INFORMATION:													
(i) APPLICANT: Gately, Maurice K. Presky, David H.													
(ii) TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN IL-12													
(iii) NUMBER OF SEQUENCES: 4 (iv) CORRESPONDENCE ADDRESS:													
(A) ADDRESSEE: Hoffmann-La Roche Inc. (B) STREET: 340 Kingsland Street													
(C) CITY: Nutley													
(D) STATE: New Jersey													
(E) COUNTRY: United States (F) ZIP: 07110-1199													
(v) COMPUTER READABLE FORM:													
(A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible													
(C) OPERATING SYSTEM: PC-DOS/MS-DOS(D) SOFTWARE: PatentIn Release #1.0, Version #1.25													
(vi) CURRENT APPLICATION DATA:													
(A) APPLICATION NUMBER: US/09/652,282 (B) FILING DATE: 30-Aug-2000													
(C) CLASSIFICATION: <unknown></unknown>													
<pre>(vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 09/232,522</pre>													
(B) FILING DATE: <unknown></unknown>													
(viii) ATTORNEY/AGENT INFORMATION: (A) NAME: Buchholz, Briana C.													
(B) REGISTRATION NUMBER: 39,123													
(C) REFERENCE/DOCKET NUMBER: CD 1048P (ix) TELECOMMUNICATION INFORMATION:													
(A) TELEPHONE: 973-235-6208													
(B) TELEFAX: 973-235-2363 (2) INFORMATION FOR SEQ ID NO: 1:													
(i) SEQUENCE CHARACTERISTICS:													
(A) LENGTH: 321 base pairs (B) TYPE: nucleic acid													
(C) STRANDEDNESS: double													
(D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA													
(iii) HYPOTHETICAL: NO													
(iv) ANTI-SENSE: NO (vi) ORIGINAL SOURCE:													
(A) ORGANISM: mouse													
(G) CELL TYPE: Hybridoma (H) CELL LINE: HIL-12F3-16G2													
(ix) FEATURE:													
(A) NAME/KEY: CDS (B) LOCATION: 1321													
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	40												
CTG GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser	48												
1 5 10 15 CTC ACC TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC	06												
Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn	96												
20 25 30 TGG ATC CGG AAA TTC CCA GGG AAT AAA TTT GAG TAC ATG GGA TTC ATA	144												
Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile	144												
35 40 45 AGT TAT AGT GGT AGC ACT TAC AAT AAT CCA TCT CTC AAA AAT CGA GTC	192												
Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val													
50 55 60 TCC ATC ACT CGA GAC ACA TCC AAT AAC CAG TAC TAC CTG CAG TTG AGT	240												
Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser	270												
65 70 75 80													

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	US09652282.txt TCT GTG ACT ACT GAG GAC TCA GCC ACA TAT TAC TGT GCA AGA TCT TCG 2																	
								GCC Ala										288
					TAC			GCA Ala										321
(2) I		SEQUAL (A)	JENCI) LEI) TYI	FOR S E CHANGTH: PE: 6	ARAC 107 aming	TERIS 7 am 5 ac	STICS ino a id		5									
	ii)) MOLECULE TYPE: protein) SEQUENCE DESCRIPTION: SEQ ID NO: 2:																
(X1) Leu 1	SEQI Glu	Glu Glu	Ser	SCRII Gly 5	PTION Pro	N: SI Ser	EQ II Leu	Val	: 2: Lys 10	Pro	Ser	Gln	Thr	Leu 15	Ser		
	Leu	Thr	Cys	Ser 20	٧aĺ	Thr	Gly	Asp	Ser 25	Ile	Thr	Ser	Gly	Tyr		Asn		
	Trp	Ile	Arg		Phe	Pro	Gly	Asn	Lys	Phe	Glu	Tyr	Met	Gly	Phe	Ile		
	Ser	Tyr 50	ser	Gly	Ser	Thr	Tyr 55	Asn	Asn	Pro	Ser	Leu 60	Lys	Asn	Arg	٧a٦		
	Ser 65	Ile	Thr	Arg	Asp	Thr 70	Ser	Asn	Asn	Gln	Tyr 75	Tyr	Leu	Gln	Leu	Ser 80		
		۷al	Thr	Thr	Glu 85		Ser	Ala	Thr	Tyr	Tyr	Cys	Ala	Arg	ser 95			
	Asp	Ala	Leu	Asp 100		Trp	Gly	Ala	Gly 105	Thr	Thr				9)			
(2) I	NEOE	мата	TON I	FOR S	EO 1	ED NO) · 2											
(-) -		SEQUAL (A)	JENCI) LEI) TYI) STI	E CHANGTH: PE: r RANDE	ARACT : 308 nucle EDNES	TERIS B bas eic a SS: 0	STICS Se pa acid doub	s: airs										
(i	ii)	MOLE HYPO	CULE OTHE	Ξ ΤΥΙ ΓΙCΑΙ NSE:	PE: (DNA	41											
(vi)	(A) (G)	OR(SOU SANIS L TY	SM: n /PE:	nouse Hybi	⁻i dor	na 3-20E	:11									
(ix)	FEAT	TURE:					, 201										
,		(B)	LO	CATIO	ON: 1	L30												
	GAG	GAG	TCA	GGA	CCT	AGC	CTC	EQ II GTG Val	AAA	CCT	TCT	CAG	ACT	CTG	TCC	СТС		48
	1				5					10					15			0.0
	Thr	Cys	Ser	val 20	Thr	Gly	Asp	TCC Ser	Ile 25	Thr	Ser	Gly	Tyr	Trp 30	Asn	Trp		96
	ATC Ile	CGG Arg	AAA Lys 35	TTC Phe	CCA Pro	GAT Asp	AAT Asn	ACA Thr 40	CTT Leu	GAG Glu	TAC Tyr	ATG Met	GGA Gly	TAC Tyr	ATA Ile	AGT Ser		144
	TAC Tyr	AGT Ser 50	GGT	AGT Ser	ACT Thr	TAC Tyr	TAC Tyr	AAT Asn	CCA Pro	TCT Ser	CTC Leu	Arg	AGT Ser	CGA Arg	ATC Ile	TCC Ser		192
	ATC Ile 65	ACT	CGA Arg	GAC Asp	ACA Thr	Ser	AAG Lys	AAC Asn	CAG Gln	TAC Tyr	Ser	ATG Met	CAG Gln	TTG Leu	AAT Asn	Ser		240
	GTG	ACT Thr	ACT Thr	GAG Glu	GAC Asp	70 ACA Thr	GCC Ala	ACA Thr	Tyr	TAC Tyr age 2	Cys	GCA Ala	AGA Arg	TCC Ser	TCG Ser	80 GAT Asp		288
									70	yc 2	-							

95

308

GCT ATG GAC TAC TGG GGC GC Ala Met Asp Tyr Trp Gly 100

(2) INFORMATION FOR SEQ ID NO: 4: (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu 10 15

Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp 20 25

Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser 35

Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser 50 55

Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Ser Met Gln Leu Asn Ser 65

Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Ser Asp 90

Ala Met Asp Tyr Trp Gly 100